

#2

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/854,883

DATE: 06/05/2001

TIME: 08:27:24

Input Set : A:\es.txt

Output Set: C:\CRF3\06052001\I854883.raw

P.S.
ENTERED

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4 <110> APPLICANT: Lex M. Cowsert
5      Jacqueline Wyatt
6      Susan M. Freier
7      Brett P. Monia
8      Madeline M. Butler
9      Robert McKay
11 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
13 <130> FILE REFERENCE: ISPH-0576
C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/854,883
C--> 15 <141> CURRENT FILING DATE: 2001-05-14
15 <150> PRIOR APPLICATION NUMBER: US 09/629,644
16 <151> PRIOR FILING DATE: 2000-07-31
18 <150> PRIOR APPLICATION NUMBER: US 09/487,368
19 <151> PRIOR FILING DATE: 2000-01-18
21 <160> NUMBER OF SEQ ID NOS: 389
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24 <211> LENGTH: 20
25 <212> TYPE: DNA
26 <213> ORGANISM: Artificial Sequence
28 <220> FEATURE:
31 <223> OTHER INFORMATION: Antisense Oligonucleotide
33 <400> SEQUENCE: 1
34 tccgtcatcg ctcctcaggg                               20
37 <210> SEQ ID NO: 2
38 <211> LENGTH: 20
39 <212> TYPE: DNA
40 <213> ORGANISM: Artificial Sequence
42 <220> FEATURE:
45 <223> OTHER INFORMATION: Antisense Oligonucleotide
47 <400> SEQUENCE: 2
48 atgcattctg cccccaagga                               20
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51 <211> LENGTH: 3247
52 <212> TYPE: DNA
53 <213> ORGANISM: Homo sapiens
55 <220> FEATURE:
56 <221> NAME/KEY: CDS
57 <222> LOCATION: (91)...(1398)
59 <400> SEQUENCE: 3
60 gggcgggcct cggggctaag agcgcgacgc ctagagcggc agacggcgca gtgggccgag   60
62 aaggaggcgc agcagccgcc ctggcccgtc  atg gag atg gaa aag gag ttc gag   114
63                                     Met Glu Met Glu Lys Glu Phe Glu
64                                     1           5
66 cag atc gac aag tcc ggg agc tgg gcg gcc att tac cag gat atc cga   162
67 Gln Ile Asp Lys Ser Gly Ser Trp Ala Ala Ile Tyr Gln Asp Ile Arg
68     10           15           20
69 cat gaa gcc agt gac ttc cca tgt aga gtg gcc aag ctt cct aag aac   210

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70 His Glu Ala Ser Asp Phe Pro Cys Arg Val Ala Lys Leu Pro Lys Asn
71 25 30 35 40
73 aaa aac cga aat agg tac aga gac gtc agt ccc ttt gac cat agt cgg 258
74 Lys Asn Arg Asn Arg Tyr Arg Asp Val Ser Pro Phe Asp His Ser Arg
75 45 50 55
77 att aaa cta cat caa gaa gat aat gac tat atc aac gct agt ttg ata 306
78 Ile Lys Leu His Gln Glu Asp Asn Asp Tyr Ile Asn Ala Ser Leu Ile
79 60 65 70
81 aaa atg gaa gaa gcc caa agg agt tac att ctt acc cag ggc cct ttg 354
82 Lys Met Glu Glu Ala Gln Arg Ser Tyr Ile Leu Thr Gln Gly Pro Leu
83 75 80 85
85 cct aac aca tgc ggt cac ttt tgg gag atg gtg tgg gag cag aaa agc 402
86 Pro Asn Thr Cys Gly His Phe Trp Glu Met Val Trp Glu Gln Lys Ser
87 90 95 100
89 agg ggt gtc gtc atg ctc aac aga gtg atg gag aaa ggt tgc tta aaa 450
90 Arg Gly Val Val Met Leu Asn Arg Val Met Glu Lys Gly Ser Leu Lys
91 105 110 115 120
93 tgc gca caa tac tgg cca caa aaa gaa gaa aaa gag atg atc ttt gaa 498
94 Cys Ala Gln Tyr Trp Pro Gln Lys Glu Glu Lys Glu Met Ile Phe Glu
95 125 130 135
97 gac aca aat ttg aaa tta aca ttg atc tct gaa gat atc aag tca tat 546
98 Asp Thr Asn Leu Lys Leu Thr Leu Ile Ser Glu Asp Ile Lys Ser Tyr
99 140 145 150
101 tat aca gtg cga cag cta gaa ttg gaa aac ctt aca acc caa gaa act 594
102 Tyr Thr Val Arg Gln Leu Glu Leu Glu Asn Leu Thr Thr Gln Glu Thr
103 155 160 165
105 cga gag atc tta cat ttc cac tat acc aca tgg cct gac ttt gga gtc 642
106 Arg Glu Ile Leu His Phe His Tyr Thr Thr Trp Pro Asp Phe Gly Val
107 170 175 180
109 cct gaa tca cca gcc tca ttc ttg aac ttt ctt ttc aaa gtc cga gag 690
110 Pro Glu Ser Pro Ala Ser Phe Leu Asn Phe Leu Phe Lys Val Arg Glu
111 185 190 195 200
113 tca ggg tca ctc agc ccg gag cac ggg ccc gtt gtg gtg cac tgc agt 738
114 Ser Gly Ser Leu Ser Pro Glu His Gly Pro Val Val Val His Cys Ser
115 205 210 215
117 gca ggc atc ggc agg tct gga acc ttc tgt ctg gct gat acc tgc ctc 786
118 Ala Gly Ile Gly Arg Ser Gly Thr Phe Cys Leu Ala Asp Thr Cys Leu
119 220 225 230
121 ctg ctg atg gac aag agg aaa gac cct tct tcc gtt gat atc aag aaa 834
122 Leu Leu Met Asp Lys Arg Lys Asp Pro Ser Ser Val Asp Ile Lys Lys
123 235 240 245
125 gtg ctg tta gaa atg agg aag ttt cgg atg ggg ttg atc cag aca gcc 882
126 Val Leu Leu Glu Met Arg Lys Phe Arg Met Gly Leu Ile Gln Thr Ala
127 250 255 260
128 gac cag ctg cgc ttc tcc tac ctg gct gtg atc gaa ggt gcc aaa ttc 930
129 Asp Gln Leu Arg Phe Ser Tyr Leu Ala Val Ile Glu Gly Ala Lys Phe
130 265 270 275 280
132 atc atg ggg gac tct tcc gtg cag gat cag tgg aag gag ctt tcc cac 978
133 Ile Met Gly Asp Ser Ser Val Gln Asp Gln Trp Lys Glu Leu Ser His

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134          285          290          295
136 gag gac ctg gag ccc cca ccc gag cat atc ccc cca cct ccc cgg cca 1026
137 Glu Asp Leu Glu Pro Pro Pro Glu His Ile Pro Pro Pro Pro Arg Pro
138          300          305          310
140 ccc aaa cga atc ctg gag cca cac aat ggg aaa tgc agg gag ttc ttc 1074
141 Pro Lys Arg Ile Leu Glu Pro His Asn Gly Lys Cys Arg Glu Phe Phe
142          315          320          325
144 cca aat cac cag tgg gtg aag gaa gag acc cag gag gat aaa gac tgc 1122
145 Pro Asn His Gln Trp Val Lys Glu Glu Thr Gln Glu Asp Lys Asp Cys
146          330          335          340
148 ccc atc aag gaa gaa aaa gga agc ccc tta aat gcc gca ccc tac ggc 1170
149 Pro Ile Lys Glu Glu Lys Gly Ser Pro Leu Asn Ala Ala Pro Tyr Gly
150          345          350          355          360
152 atc gaa agc atg agt caa gac act gaa gtt aga agt cgg gtc gtg ggg 1218
153 Ile Glu Ser Met Ser Gln Asp Thr Glu Val Arg Ser Arg Val Val Gly
154          365          370          375
156 gga agt ctt cga ggt gcc cag gct gcc tcc cca gcc aaa ggg gag cgg 1266
157 Gly Ser Leu Arg Gly Ala Gln Ala Ala Ser Pro Ala Lys Gly Glu Pro
158          380          385          390
160 tca ctg ccc gag aag gac gag gac cat gca ctg agt tac tgg aag ccc 1314
161 Ser Leu Pro Glu Lys Asp Glu Asp His Ala Leu Ser Tyr Trp Lys Pro
162          395          400          405
164 ttc ctg gtc aac atg tgc gtg gct acg gtc ctc acg gcc ggc gct tac 1362
165 Phe Leu Val Asn Met Cys Val Ala Thr Val Leu Thr Ala Gly Ala Tyr
166          410          415          420
168 ctc tgc tac agg ttc ctg ttc aac agc aac aca tag cctgaccctc 1408
169 Leu Cys Tyr Arg Phe Leu Phe Asn Ser Asn Thr
170          425          430          435
172 ctccactcca cctccaccca ctgtccgcct ctgcccgcag agcccaacgcc cgactagcag 1468
174 gcatgccgcg gtaggtaagg gccgccggac cgcgtagaga gccggggcccc ggacggacgt 1528
176 tggttcttga ctaaaaccca tcttccccgg atgtgtgtct caccctcat ccttttactt 1588
178 tttgcccttt ccactttgag taccaaatcc acaagccatt ttttgaggag agtgaaagag 1648
180 agtaccatgc tggcggcgca gagggaaggg gcctacaccc gtcttggggc tcgccccacc 1708
182 cagggctccc tctggagca tcccaggcgg cgcacgcaa cagccccccc cttgaatctg 1768
184 cagggagcaa ctctccactc catatttatt taaacaattt tttcccaaa ggcatccata 1828
186 gtgcactagc attttcttga accaataatg tattaataat ttttgatgtc agccttgcac 1888
187 caagggtttt atcaaaaagt acaataataa atcctcaggt agtactggga atggaaggct 1948
189 ttgccatggg cctgctgcgt cagaccagta ctgggaagga ggacggttgt aagcagttgt 2008
191 tatttagtga tattgtgggt aacgtgagaa gatagaacaa tgctataata tataatgaac 2068
193 acgtgggtat ttaataagaa acatgatgtg agattacttt gtcccgttta ttctctccc 2128
195 tgttatctgc tagatctagt tctcaatcac tgctcccccg tgtgtattag aatgcatgta 2188
197 aggtcttctt gtgtcctgat gaaaaatatg tgcttgaaat gagaaacttt gatctctgct 2248
199 tactaatgtg ccccatgtcc aagtccaacc tgctgtgca tgacctgac attacatggc 2308
201 tgtggttctt aagcctgttg ctgaagtcac tgcgtcag caataggggt cagttttcca 2368
203 ggaataggca tttgctaatt cctggcatga cactctagt acttctcgtt gaggccacc 2428
205 ctgtcctggt acagcagggt cttgctgtaa ctgagacatt ccaagggtat gggaagccat 2488
207 attcacacct cagcctctgg acatgattta gggaagcagg gacaccccc gcccccacc 2548
209 tttgggatca gcctccgcca ttccaagtca acactctct tgagcagacc gtgatttgga 2608
211 agagaggcac ctgctggaac ccacacttct tgaaacagcc tgggtgacgg tcctttaggc 2668

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213 agcctgccgc cgtctctgtc ccggttcacc ttgccgagag aggcgcgtct gccccaccct 2728
215 caaacctgt ggggcctgat ggtgctcacg actcttcctg caaagggaac tgaagacctc 2788
217 cacattaagt ggctttttaa catgaaaaac acggcagctg tagctcccga gctactctct 2848
219 tgccagcatt ttcacatttt gcctttctcg tggtagaagc cagtacagag aaattctgtg 2908
221 gtgggaacat tgcagggtgc accctgcaga gctatggtga ggtgtggata aggcttaggt 2968
223 gccaggctgt aagcattctg agctggcttg ttgtttttaa gtcctgtata tgtatgtagt 3028
225 agtttgggtg tgtatatata gtagcatttc aaaatggacg tactggttta acctcctatc 3088
227 cttggagagc agctggctct ccaccttggt acacattatg ttagagaggt agcgagctgc 3148
229 tctgctatat gccttaagcc aatatttact catcagggtca ttatttttta caatggccat 3208
231 ggaataaacc atttttataa aaataaaaac aaaaaaagc 3247
234 <210> SEQ ID NO: 4
235 <211> LENGTH: 21
236 <212> TYPE: DNA
237 <213> ORGANISM: Artificial Sequence
239 <220> FEATURE:
242 <223> OTHER INFORMATION: PCR Primer
244 <400> SEQUENCE: 4
245 ggagttcgag cagatcgaca a
248 <210> SEQ ID NO: 5 21
249 <211> LENGTH: 21
250 <212> TYPE: DNA
251 <213> ORGANISM: Artificial Sequence
253 <220> FEATURE:
256 <223> OTHER INFORMATION: PCR Primer
258 <400> SEQUENCE: 5
259 gccactcta catgggaagt c
262 <210> SEQ ID NO: 6 21
263 <211> LENGTH: 24
264 <212> TYPE: DNA
265 <213> ORGANISM: Artificial Sequence
267 <220> FEATURE:
270 <223> OTHER INFORMATION: PCR Probe
272 <400> SEQUENCE: 6
273 agctgggagg ccatttacca ggat
276 <210> SEQ ID NO: 7 24
277 <211> LENGTH: 19
278 <212> TYPE: DNA
279 <213> ORGANISM: Artificial Sequence
281 <220> FEATURE:
284 <223> OTHER INFORMATION: PCR Primer
286 <400> SEQUENCE: 7
287 gaaggtgaag gtcggagtc
290 <210> SEQ ID NO: 8 19
291 <211> LENGTH: 20
292 <212> TYPE: DNA
293 <213> ORGANISM: Artificial Sequence
295 <220> FEATURE:
298 <223> OTHER INFORMATION: PCR Primer
300 <400> SEQUENCE: 8

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Input Set : A:\es.txt

Output Set: C:\CRF3\06052001\I854883.raw

301 gaagatggtg atgggatttc
 304 <210> SEQ ID NO: 9 20
 305 <211> LENGTH: 20
 306 <212> TYPE: DNA
 307 <213> ORGANISM: Artificial Sequence
 309 <220> FEATURE:
 312 <223> OTHER INFORMATION: PCR Probe
 314 <400> SEQUENCE: 9
 315 caagcttccc gttctcagcc
 318 <210> SEQ ID NO: 10 20
 319 <211> LENGTH: 4127
 320 <212> TYPE: DNA
 321 <213> ORGANISM: Rattus norvegicus
 323 <220> FEATURE:
 324 <221> NAME/KEY: CDS
 325 <222> LOCATION: (120)...(1418)
 327 <400> SEQUENCE: 10
 328 agccgctgct ggggaggttg gggctgaggt ggtggcgggc gacgggcctc gagacgcgga 60
 330 ggcacgcggc ctagcgccgc ggacggccga ggggaactcg gcagtcgtcc cgtcccgcc 119
 334 atg gaa atg gag aag gaa ttc gag cag atc gat aag gct ggg aac tgg 167
 335 Met Glu Met Glu Lys Glu Phe Glu Gln Ile Asp Lys Ala Gly Asn Trp
 336 1 5 10 15
 338 gcg gct att tac cag gat att cga cat gaa gcc agt gac ttc cca tgc 215
 339 Ala Ala Ile Tyr Gln Asp Ile Arg His Glu Ala Ser Asp Phe Pro Cys
 340 20 25 30
 342 aga ata gcg aaa ctt cct aag aac aaa aac cgg aac agg tac cga gat 263
 343 Arg Ile Ala Lys Leu Pro Lys Asn Lys Asn Arg Asn Arg Tyr Arg Asp
 344 35 40 45
 346 gtc agc cct ttt gac cac agt cgg att aaa ttg cat cag gaa gat aat 311
 347 Val Ser Pro Phe Asp His Ser Arg Ile Lys Leu His Gln Glu Asp Asn
 348 50 55 60
 350 gac tat atc aat gcc agc ttg ata aaa atg gag gaa gcc cag agg agc 359
 351 Asp Tyr Ile Asn Ala Ser Leu Ile Lys Met Glu Glu Ala Gln Arg Ser
 352 65 70 75 80
 354 tat atc ctc acc cag ggc cct tta cca aac acg tgc ggg cac ttc tgg 407
 355 Tyr Ile Leu Thr Gln Gly Pro Leu Pro Asn Thr Cys Gly His Phe Trp
 356 85 90 95
 358 gag atg gtg tgg gag cag aag agc agg ggc gtg gtc atg ctc aac cgc 455
 359 Glu Met Val Trp Glu Gln Lys Ser Arg Gly Val Val Met Leu Asn Arg
 360 100 105 110
 362 atc atg gag aaa ggc tcg tta aaa tgt gcc cag tat tgg cca cag aaa 503
 363 Ile Met Glu Lys Gly Ser Leu Lys Cys Ala Gln Tyr Trp Pro Gln Lys
 364 115 120 125
 366 gaa gaa aaa gag atg gtc ttc gat gac acc aat ttg aag ctg aca ctg 551
 367 Glu Glu Lys Glu Met Val Phe Asp Asp Thr Asn Leu Lys Leu Thr Leu
 368 130 135 140
 370 atc tct gaa gat gtc aag tca tat tac aca gta cgg cag ttg gag ttg 599
 371 Ile Ser Glu Asp Val Lys Ser Tyr Tyr Thr Val Arg Gln Leu Glu Leu
 372 145 150 155 160

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

6/5/01

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/854,883

DATE: 06/05/2001

TIME: 08:27:25

Input Set : A:\es.txt

Output Set: C:\CRF3\06052001\I854883.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application No
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:567 M:283 W: Missing Blank Line separator, <220> field identifier
L:639 M:283 W: Missing Blank Line separator, <400> field identifier
L:3886 M:283 W: Missing Blank Line separator, <220> field identifier
L:3890 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:242